



/600

16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/559,013E

DATE: 10/09/2003
TIME: 15:21:52

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Input Set : A:\L0461-70086US00.txt
Output Set: N:\CRF4\10092003\I559013E.raw

3 <110> APPLICANT: Ono, Toshiro
4 Nakayama, Eiichi
6 <120> TITLE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES THEREFOR
8 <130> FILE REFERENCE: L0461.70086US00
10 <140> CURRENT APPLICATION NUMBER: US 09/559,013E
11 <141> CURRENT FILING DATE: 2000-04-26
13 <150> PRIOR APPLICATION NUMBER: US 60/168,353
14 <151> PRIOR FILING DATE: 1999-12-01
16 <160> NUMBER OF SEQ ID NOS: 33
18 <170> SOFTWARE: PatentIn Version 3.2

ENTERED

20 <210> SEQ ID NO: 1
21 <211> LENGTH: 538
22 <212> TYPE: DNA
23 <213> ORGANISM: Mus musculus
25 <400> SEQUENCE: 1
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27 tatctgcgtc ggggagagcg gagacagact gaccgggca gccaaaggtgt tggagcagct 120
28 cacaggccag accccggtgt tctccaaagc tagatacact gtcaggtcct ttggcatccg 180
29 gagaaatgag aagattgctg ttcactgcac agtccgcgga gccaaaggcag aggaaattct 240
30 ggagaaaggc ctgaagggtgc gggagtatga gttgcggaaa aataacttct cggatactgg 300
31 aaactttggt tttggaattc aagaacacat tgacctgggc atcaaatacg acccaagcat 360
32 tgggatctac ggcctggact tctatgtggt gctgggtagg ccagggttca gcatcgaga 420
33 caagaagcgc agaacaggct gcattggggc caaacacaga atcagcaagg aggaggccat 480
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37 <211> LENGTH: 175
38 <212> TYPE: PRT
39 <213> ORGANISM: Mus musculus
41 <400> SEQUENCE: 2
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43 1 5 10 15
44 Leu Cys Leu Asn Ile Cys Val Gly Glu Ser Gly Asp Arg Leu Thr Arg
45 20 25 30
46 Ala Ala Lys Val Leu Glu Gln Leu Thr Gly Gln Thr Pro Val Phe Ser
47 35 40 45
48 Lys Ala Arg Tyr Thr Val Arg Ser Phe Gly Ile Arg Arg Asn Glu Lys
49 50 55 60
50 Ile Ala Val His Cys Thr Val Arg Gly Ala Lys Ala Glu Glu Ile Leu
51 65 70 75 80
52 Glu Lys Gly Leu Lys Val Arg Glu Tyr Glu Leu Arg Lys Asn Asn Phe
53 85 90 95
54 Ser Asp Thr Gly Asn Phe Gly Phe Gly Ile Gln Glu His Ile Asp Leu
55 100 105 110

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56 Gly Ile Lys Tyr Asp Pro Ser Ile Gly Ile Tyr Gly Leu Asp Phe Tyr
57      115      120      125
58 Val Val Leu Gly Arg Pro Gly Phe Ser Ile Ala Asp Lys Lys Arg Arg
59      130      135      140
60 Thr Gly Cys Ile Gly Ala Lys His Arg Ile Ser Lys Glu Glu Ala Met
61      145      150      155      160
62 Arg Trp Phe Gln Gln Lys Tyr Asp Gly Ile Ile Leu Pro Gly Lys
63      165      170      175
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66 <211> LENGTH: 1228
67 <212> TYPE: DNA
68 <213> ORGANISM: Mus musculus
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73 agtggagatt gttgccatca acgaccctt cattgacctc aactacatgg tctacatggt 180
74 ccagtatgac tccactcacg gcaaatcaaa cggcacagtc aaggccgaga atgggaagct 240
75 tgtcatcaac gggaagccca tcaccatctt ccaggagcga gacccacta acatcaaagt 300
76 gggtgaggcc ggtgctgagt atgtcgtgga gtctactggg gtcttcacca ccatggagaa 360
77 ggccggggcc cacttgaagg gtggagccaa acgggtcatc atctccgccc cttctgccga 420
78 tgcccccatg tttgtgatgg gtgtgaacca cgagaaatat gacaactcac tcaagattgt 480
79 cagcaatgca tcctgcacca ccaactgctt agccccctg gccaaagtca tccatgacaa 540
80 ctttggcatt gtggaagggc tcatgaccac agtccatgcc atcactgcca cccagaagac 600
81 tgttgatggc ccctctggaa agctgtggcg tgatggcgtg ggggctgccc agaaccatcat 660
82 ccctgcattc actggtgctg ccaaggctgt gggcaaggtc atcccagagc tgaacgggaa 720
83 gctcactggc atggccttcc gtgttcttac cccaatgtg tccgtcgtgg atctgacgtg 780
84 ccgcctggag aaacctgcca agtatgatga catcaagaag gtggtgaagc aggcattctga 840
85 gggccactg aaggcatct tgggctacac tgaggaccag gttgtctcct gcgacttcaa 900
86 cagcaactcc cactcttcca cttcgtatgc cggggtggtc attgctctca atgacaactt 960
87 tgtcaagctc atttcttgt atgacaatga atacggctac agcaacaggg tgggtggacct 1020
88 catggcctac atggcctcca aggagtaaga aacctggac caccacccc agcaaggaca 1080
89 ctgagcaaga gaggcctat cccaactcgg cccccaacac tgagcatctc cctcacaatt 1140
90 tccatcccag acccccataa taacaggagg ggcctaggga gccctcccta ctctcttgaa 1200
91 taccatcaat aaagttcgct gcaccac 1228
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94 <211> LENGTH: 333
95 <212> TYPE: PRT
96 <213> ORGANISM: Mus musculus
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100 1 5 10 15
101 Thr Arg Ala Ala Ile Cys Ser Gly Lys Val Glu Ile Val Ala Ile Asn
102 20 25 30
103 Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln Tyr Asp
104 35 40 45
105 Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu Asn Gly Lys
106 50 55 60
107 Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro
108 65 70 75 80

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109 Thr Asn Ile Lys Trp Gly Glu Ala Gly Ala Glu Tyr Val Val Glu Ser
110      85      90      95
111 Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu Lys Gly
112      100      105      110
113 Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met
114      115      120      125
115 Phe Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu Lys Ile
116      130      135      140
117 Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys
118      145      150      155      160
119 Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr Thr Val
120      165      170      175
121 His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser Gly Lys
122      180      185      190
123 Leu Trp Arg Asp Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Ala Ser
124      195      200      205
125 Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly
126      210      215      220
127 Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asn Val Ser Val
128      225      230      235      240
129 Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile
130      245      250      255
131 Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly Ile Leu
132      260      265      270
133 Gly Tyr Thr Glu Asp Gln Val Val Ser Cys Asp Phe Asn Ser Asn Ser
134      275      280      285
135 His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn Asp Asn
136      290      295      300
137 Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr Ser Asn
138      305      310      315      320
139 Arg Val Val Asp Leu Met Ala Tyr Met Ala Ser Lys Glu
140      325      330

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142 <210> SEQ ID NO: 5

143 <211> LENGTH: 1705

144 <212> TYPE: DNA

145 <213> ORGANISM: Mus musculus

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148 <221> NAME/KEY: Unsure

149 <222> LOCATION: (611)..(611)

150 <223> OTHER INFORMATION: n = a, c, g, or t

152 <220> FEATURE:

153 <221> NAME/KEY: Unsure

154 <222> LOCATION: (730)..(730)

155 <223> OTHER INFORMATION: n = a, c, g, or t

157 <220> FEATURE:

158 <221> NAME/KEY: Unsure

159 <222> LOCATION: (746)..(746)

160 <223> OTHER INFORMATION: n = a, c, g, or t

162 <220> FEATURE:

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164 <222> LOCATION: (755)..(755)
165 <223> OTHER INFORMATION: n = a, c, g, or t
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169 <222> LOCATION: (1288)..(1288)
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172 <220> FEATURE:
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174 <222> LOCATION: (1318)..(1318)
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177 <220> FEATURE:
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180 <223> OTHER INFORMATION: n = a, c, g, or t
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184 ctgctgggtg cattccacaa cacaaaacag gtgacaagag gttttgctgg tgggtgttcag 120
185 acagtaactt taattccttg agatggaatt ggcccagaaa tttcagcctc agtcatgaag 180
186 atttttgatg ctgccaaagc acctattcag tgggaggagc gcaatgtcac agcaattcaa 240
187 ggaccaggag gaaagtggat gatccctcca gaagccaagg agtccatgga taagaacaag 300
188 atgggcttga aaggcccact aaagacccca atagccgctg gccatccatc tatgaatctg 360
189 ttgcttcgta agacatttga cctttatgcc aatgtccggc catgtgtctc aattgaaggt 420
190 tataaaaccc cttacacgga tgtaaatatc gtcaccatcc gagagaacac ggaaggagaa 480
191 tacagtggaa ttgagcatgt gatcgttgat ggggttgtgc agagcatcaa gctcatcacc 540
192 gaagaagcaa gcaagcgcat tgcagagttt gcttcgagta cgctcggaac aaccaccgga 600
> 193 accacgtcac ngctgtgcac aaaagctaac atcatgagga tgtcagatgg gctctttctg 660
194 caaaaatgca gggaaatttg cggaagaact gtaaagactt aaatttaacg agatgtactt 720
195 ggatactgtg gtttaaatat ggggtanaaa acccntccaa tttgatgttc ttgtcatgcc 780
196 aaattttatac ggagacatcc ttagtgatct gtgtgcagga ctgattggag gtcttggggg 840
197 gactccaagt ggcaatattg gagccaacgg tgttgccatc tttgaatcgg ttcattggaac 900
198 agccccggac attgcaggca aggacatggc caaccccacg gccctcctgc ttagtgctgt 960
199 gatgatgctt cgccacatgg gactttttga ccatgcagca aaaatcgagg ctgcatgttt 1020
200 tgctacaatt aaggatggaa agagcttaac aaaagatctg ggaggcaacg cgaagtgtct 1080
201 tgacttcaca gaagaaatct gtcgtagagt caaagactta gattagcact cctgctgggt 1140
202 gatttgctgc agtcagtcaa tcaactccaa aggataccct gtaatcctcc ttgagggcgc 1200
203 ccaccattgg tttgcttggg tcttgacaga gtacgttttt tgaatctggc cttttcttaa 1260
204 caaaaccctt tgcaatggat gcacatgntg gccccaggcc tttcattcaa aaggtttncc 1320
205 ccaagtgtct gtggtattta ttgtcccgtc tgggtaaaacn ttattttgta aactgtaagt 1380
206 gaactgtatc atttatcatt gtaaacccat ttacacttc aggcaaaatc attttcctca 1440
207 actgtaataa ttctgtatca gaattaataa gagaagatat ttaacttttt aacaaaagcc 1500
208 ctggattttt ggtttatgaa aaacaaactg ggaataaaac agggttttta caatcgaca 1560
209 agataacatt attctaatac taatgggtac aaaagaaatt tactgggaaa gttcacagca 1620
210 aaaaaatggt atatttctta aaaatatgga aataaagtat ttgtcctata catgaattac 1680
211 tattaataaa aatgtaagct ccaag 1705
213 <210> SEQ ID NO: 6
214 <211> LENGTH: 233
215 <212> TYPE: PRT
216 <213> ORGANISM: Mus musculus

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218 <220> FEATURE:
220 <221> NAME/KEY: UNSURE
222 <222> LOCATION: (204)..(204)
224 <223> OTHER INFORMATION: Xaa = any amino acid
226 <400> SEQUENCE: 6
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228 1 5 10 15
229 Lys Val Ser Arg Leu Leu Gly Ala Phe His Asn Thr Lys Gln Val Thr
230 20 25 30
231 Arg Gly Phe Ala Gly Gly Val Gln Thr Val Thr Leu Ile Pro Gly Asp
232 35 40 45
233 Gly Ile Gly Pro Glu Ile Ser Ala Ser Val Met Lys Ile Phe Asp Ala
234 50 55 60
235 Ala Lys Ala Pro Ile Gln Trp Glu Glu Arg Asn Val Thr Ala Ile Gln
236 65 70 75 80
237 Gly Pro Gly Gly Lys Trp Met Ile Pro Pro Glu Ala Lys Glu Ser Met
238 85 90 95
239 Asp Lys Asn Lys Met Gly Leu Lys Gly Pro Leu Lys Thr Pro Ile Ala
240 100 105 110
241 Ala Gly His Pro Ser Met Asn Leu Leu Leu Arg Lys Thr Phe Asp Leu
242 115 120 125
243 Tyr Ala Asn Val Arg Pro Cys Val Ser Ile Glu Gly Tyr Lys Thr Pro
244 130 135 140
245 Tyr Thr Asp Val Asn Ile Val Thr Ile Arg Glu Asn Thr Glu Gly Glu
246 145 150 155 160
247 Tyr Ser Gly Ile Glu His Val Ile Val Asp Gly Val Val Gln Ser Ile
248 165 170 175
249 Lys Leu Ile Thr Glu Glu Ala Ser Lys Arg Ile Ala Glu Phe Ala Ser
250 180 185 190
> 251 Ser Thr Leu Gly Thr Thr Thr Gly Thr Thr Ser Xaa Leu Cys Thr Lys
252 195 200 205
253 Ala Asn Ile Met Arg Met Ser Asp Gly Leu Phe Leu Gln Lys Cys Arg
254 210 215 220
255 Glu Ile Cys Gly Arg Thr Val Lys Thr
256 225 230
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259 <211> LENGTH: 853
260 <212> TYPE: DNA
261 <213> ORGANISM: Mus musculus
263 <400> SEQUENCE: 7
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265 ctctgtcctt ccgtggacaa gaggaagcac aaagaatcat ccaggtatgg aagctgaggg 120
266 ttccagccgc aaggtcacca ggctactccg cctgggagtc aaggaagact cggaagaaca 180
267 gcatgatgtg aaagcagagg ctttcttcca ggctggagag gggagagatg agcaaggtgc 240
268 acagggccag cctggagtgg gagcgggtgg aacagaaggc gaaggagaag aattaaatgg 300
269 aggaaaaggc cacttttggtc ctggtgctcc tggctctatg ggtgatgggg acaaggatag 360
270 tggcaccagg gctggtggtg tggagcagga acaaaatgag ccagttgctg agggcactga 420
271 gagccaggag aatggaaatc ctgggggtag gcagatgcc ctccagggct ctagggttcgc 480
272 ccagcatcga ctgaggaac tggagtccat tttgcagcgc actaattcct ttgatgtccc 540

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RAW SEQUENCE LISTING ERROR SUMMARY
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ase Note:

of n and/or Xaa have been detected in the Sequence Listing. Please review the
uence Listing to ensure that a corresponding explanation is presented in the <220>
<223> fields of each sequence which presents at least one n or Xaa.

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#:6; Xaa Pos. 204

#:9; N Pos. 551,555,587,593,628,631,634,656,669,672,679,685,699,713,717

#:9; N Pos. 732,745,753,778,779,787,789,791,797,802,813,814,817,818,847

#:9; N Pos. 861,865,867,870,876,880,882

#:15; N Pos. 77